

PCT10

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/018,418

DATE: 01/09/2002

TIME: 12:12:46

Input Set : A:\127-01.app

Output Set: N:\CRF3\01082002\J018418.raw

P.S

3 <110> APPLICANT: Morell, Matthew
4 Li, Zhongyi
5 Rahman, Sadequr
6 Appels, Rudolph
8 <120> TITLE OF INVENTION: Genes Encoding Wheat Starch Synthases and Uses Therefor
10 <130> FILE REFERENCE: 127-01
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/018,418
13 <141> CURRENT FILING DATE: 2001-10-29
15 <150> PRIOR APPLICATION NUMBER: PCT AU00/00385
16 <151> PRIOR FILING DATE: 2000-04-28
18 <150> PRIOR APPLICATION NUMBER: AU PQ0052/99
19 <151> PRIOR FILING DATE: 1999-04-29
21 <160> NUMBER OF SEQ ID NOS: 54
23 <170> SOFTWARE: PatentIn Ver. 2.0
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 2939
27 <212> TYPE: DNA
28 <213> ORGANISM: Triticum aestivum
30 <220> FEATURE:
31 <221> NAME/KEY: CDS
32 <222> LOCATION: (176)..(2569)
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39 gcggaccaac ccgcgcacgc tatcacgac acccaccocg atcccgccgc ccgcc atg 178
40 Met
41 1
43 tcg tcg gcg gtc gcg tcc gcc gcg tcc ttc ctc gcg ctc gcg tcc gcc 226
44 Ser Ser Ala Val Ala Ser Ala Ala Ser Phe Leu Ala Leu Ala Ser Ala
45 5 10 15
47 tcc ccc ggg aga tca cgg agg agg acg agg gtg agc gcg tcg cca ccc 274
48 Ser Pro Gly Arg Ser Arg Arg Arg Thr Arg Val Ser Ala Ser Pro Pro
49 20 25 30
51 cac acc ggg gct ggc agg ttg cac tgg ccg ccg tcg ccg ccg cag cgc 322
52 His Thr Gly Ala Gly Arg Leu His Trp Pro Pro Pro Pro Pro Gln Arg
53 35 40 45
55 acg gct cgc gac gga gcg gtg gcc gcg cgc gcc gcc ggg aag aag gac 370
56 Thr Ala Arg Asp Gly Ala Val Ala Ala Arg Ala Ala Gly Lys Lys Asp
57 50 55 60 65
59 gcg ggg atc gac gac gcc gcg ccc gcg agg cag ccc cgc gca ctc cgc 418
60 Ala Gly Ile Asp Asp Ala Ala Pro Ala Arg Gln Pro Arg Ala Leu Arg
61 70 75 80
63 ggt ggc gcc gcc acc aag gtt gcg gag cgg agg gat ccc gtc aag acg 466
64 Gly Gly Ala Ala Thr Lys Val Ala Glu Arg Arg Asp Pro Val Lys Thr
65 85 90 95
67 ctc gat cgc gac gcc gcg gaa ggt ggc gcg ccg tcc ccg ccg gca ccg 514
68 Leu Asp Arg Asp Ala Ala Glu Gly Gly Ala Pro Ser Pro Pro Ala Pro

ENTERED

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69          100          105          110
71 agg cag gag gac gcc cgt ctg ccg agc atg aac ggc atg ccg gtg aac 562
72 Arg Gln Glu Asp Ala Arg Leu Pro Ser Met Asn Gly Met Pro Val Asn
73          115          120          125
75 ggt gaa aac aaa tct acc ggc ggc ggc ggc gcg act aaa gac agc ggg 610
76 Gly Glu Asn Lys Ser Thr Gly Gly Gly Gly Ala Thr Lys Asp Ser Gly
77 130          135          140          145
79 ctg ccc gca ccc gca cgc gcg ccc cag ccg tcg agc cag aac aga gta 658
80 Leu Pro Ala Pro Ala Arg Ala Pro Gln Pro Ser Ser Gln Asn Arg Val
81          150          155          160
83 ccg gtg aat ggt gaa aac aaa gct aac gtc gcc tcg ccg ccg acg agc 706
84 Pro Val Asn Gly Glu Asn Lys Ala Asn Val Ala Ser Pro Pro Thr Ser
85          165          170          175
87 ata gcc gag gtc gcg gct ccg gat ccc gca gct acc att tcc atc agt 754
88 Ile Ala Glu Val Ala Ala Pro Asp Pro Ala Ala Thr Ile Ser Ile Ser
89          180          185          190
91 gac aag gcg cca gag tcc gtt gtc cca gcc gag aag gcg ccg ccg tcg 802
92 Asp Lys Ala Pro Glu Ser Val Val Pro Ala Glu Lys Ala Pro Pro Ser
93          195          200          205
95 tcc ggc tca aat ttc gtg ccc tcg gct tct gct ccc ggg tct gac act 850
96 Ser Gly Ser Asn Phe Val Pro Ser Ala Ser Ala Pro Gly Ser Asp Thr
97 210          215          220          225
99 gtc agc gac gtg gaa ctt gaa ctg aag aag ggt gcg gtc att gtc aaa 898
100 Val Ser Asp Val Glu Leu Glu Leu Lys Lys Gly Ala Val Ile Val Lys
101          230          235          240
103 gaa gct cca aac cca aag gct ctt tcg ccg ccc gca gca ccc gct gta 946
104 Glu Ala Pro Asn Pro Lys Ala Leu Ser Pro Pro Ala Ala Pro Ala Val
105          245          250          255
107 caa caa gac ctt tgg gac ttc aag aaa tac att ggt ttc gag gag ccc 994
108 Gln Gln Asp Leu Trp Asp Phe Lys Lys Tyr Ile Gly Phe Glu Glu Pro
109          260          265          270
111 gtg gag gcc aag gat gat ggc cgg gct gtt gca gat gat gcg ggc tcc 1042
112 Val Glu Ala Lys Asp Asp Gly Arg Ala Val Ala Asp Asp Ala Gly Ser
113          275          280          285
115 ttc gaa cac cac cag aat cac gat tcc ggg cct ttg gca ggg gag aac 1090
116 Phe Glu His His Gln Asn His Asp Ser Gly Pro Leu Ala Gly Glu Asn
117 290          295          300          305
119 gtc atg aac gtg gtc gtc gtg gct gct gaa tgt tct ccc tgg tgc aaa 1138
120 Val Met Asn Val Val Val Ala Ala Glu Cys Ser Pro Trp Cys Lys
121          310          315          320
123 aca ggt ggt ctt gga gat gtt gcc ggt gct ttg ccc aag gct ttg gcg 1186
124 Thr Gly Gly Leu Gly Asp Val Ala Gly Ala Leu Pro Lys Ala Leu Ala
125          325          330          335
127 aag aga gga cat cgt gtt atg gtt gtg gta cca agg tat ggg gac tat 1234
128 Lys Arg Gly His Arg Val Met Val Val Val Pro Arg Tyr Gly Asp Tyr
129          340          345          350
131 gag gaa gcc tac gat gtc gga gtc cga aaa tac tac aag gct gct gga 1282
132 Glu Glu Ala Tyr Asp Val Gly Val Arg Lys Tyr Tyr Lys Ala Ala Gly
133          355          360          365

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135	cag	gat	atg	gaa	gtg	aat	tat	ttc	cat	gct	tat	atc	gat	gga	gtt	gat	1330
136	Gln	Asp	Met	Glu	Val	Asn	Tyr	Phe	His	Ala	Tyr	Ile	Asp	Gly	Val	Asp	
137	370					375					380					385	
139	ttt	gtg	ttc	att	gac	gct	cct	ctc	ttc	cga	cac	cgc	cag	gaa	gac	att	1378
140	Phe	Val	Phe	Ile	Asp	Ala	Pro	Leu	Phe	Arg	His	Arg	Gln	Glu	Asp	Ile	
141					390					395						400	
143	tat	ggg	ggc	agc	aga	cag	gaa	att	atg	aag	cgc	atg	att	ttg	ttc	tgc	1426
144	Tyr	Gly	Gly	Ser	Arg	Gln	Glu	Ile	Met	Lys	Arg	Met	Ile	Leu	Phe	Cys	
145				405					410							415	
147	aag	gcc	gct	gtc	gag	gtt	cca	tgg	cac	gtt	cca	tgc	ggc	ggg	gtc	cct	1474
148	Lys	Ala	Ala	Val	Glu	Val	Pro	Trp	His	Val	Pro	Cys	Gly	Gly	Val	Pro	
149				420				425					430				
151	tat	ggg	gat	gga	aat	ctg	gtg	ttt	att	gca	aat	gat	tgg	cac	acg	gca	1522
152	Tyr	Gly	Asp	Gly	Asn	Leu	Val	Phe	Ile	Ala	Asn	Asp	Trp	His	Thr	Ala	
153		435					440					445					
155	ctc	ctg	cct	gtc	tat	ctg	aaa	gca	tat	tac	agg	gac	cat	ggg	ttg	atg	1570
156	Leu	Leu	Pro	Val	Tyr	Leu	Lys	Ala	Tyr	Tyr	Arg	Asp	His	Gly	Leu	Met	
157	450					455					460					465	
159	cag	tac	act	cgg	tcc	att	atg	gtg	ata	cat	aac	atc	gct	cac	cag	ggc	1618
160	Gln	Tyr	Thr	Arg	Ser	Ile	Met	Val	Ile	His	Asn	Ile	Ala	His	Gln	Gly	
161				470						475						480	
163	cgt	ggc	cca	gta	gat	gag	ttc	ccg	ttc	acc	gag	ttg	cct	gag	cac	tac	1666
164	Arg	Gly	Pro	Val	Asp	Glu	Phe	Pro	Phe	Thr	Glu	Leu	Pro	Glu	His	Tyr	
165				485				490						495			
167	ctg	gaa	cac	ttc	aga	ctg	tac	gac	ccc	gtg	ggg	ggg	gaa	cac	gcc	aac	1714
168	Leu	Glu	His	Phe	Arg	Leu	Tyr	Asp	Pro	Val	Gly	Gly	Glu	His	Ala	Asn	
169			500					505					510				
171	tac	ttc	gcc	gcc	ggc	ctg	aag	atg	gcg	gac	cag	gtt	gtc	gtc	gtg	agc	1762
172	Tyr	Phe	Ala	Ala	Gly	Leu	Lys	Met	Ala	Asp	Gln	Val	Val	Val	Val	Ser	
173		515					520					525					
175	ccg	ggg	tac	ctg	tgg	gag	ctg	aag	acg	gtg	gag	ggc	ggc	tgg	ggg	ctt	1810
176	Pro	Gly	Tyr	Leu	Trp	Glu	Leu	Lys	Thr	Val	Glu	Gly	Gly	Trp	Gly	Leu	
177	530					535					540					545	
179	cac	gac	atc	ata	cgg	cag	aac	gac	tgg	aag	acc	cgc	ggc	atc	gtg	aac	1858
180	His	Asp	Ile	Ile	Arg	Gln	Asn	Asp	Trp	Lys	Thr	Arg	Gly	Ile	Val	Asn	
181				550						555						560	
183	ggc	atc	gac	aac	atg	gag	tgg	aac	ccc	gag							

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200 Gly Val Glu Ile Ile Ala Asp Ala Met Pro Trp Ile Val Ser Gln Asp
201                               630                               635                               640
203 gtg cag ctg gtc atg ctg ggc acc ggg cgc cac gac ctg gag ggc atg      2146
204 Val Gln Leu Val Met Leu Gly Thr Gly Arg His Asp Leu Glu Gly Met
205                               645                               650                               655
207 ctg cgg cac ttc gag cgg gag cac cac gac aag gtg cgc ggg tgg gtg      2194
208 Leu Arg His Phe Glu Arg Glu His His Asp Lys Val Arg Gly Trp Val
209                               660                               665                               670
211 ggg ttc tcc gtg cgg ctg gcg cac cgg atc acg gcc ggc gcc gac gcg      2242
212 Gly Phe Ser Val Arg Leu Ala His Arg Ile Thr Ala Gly Ala Asp Ala
213                               675                               680                               685
215 ctc ctc atg ccc tcc cgg ttc gag ccg tgc gga ctg aac cag ctc tac      2290
216 Leu Leu Met Pro Ser Arg Phe Glu Pro Cys Gly Leu Asn Gln Leu Tyr
217 690                               695                               700                               705
219 gcc atg gcc tac ggc acc gtc ccc gtc gtg cat gcc gtc ggt ggc ctg      2338
220 Ala Met Ala Tyr Gly Thr Val Pro Val Val His Ala Val Gly Gly Leu
221                               710                               715                               720
223 agg gac acc gtg ccg ccg ttc gac ccc ttc aac cac tcc ggg ctc ggg      2386
224 Arg Asp Thr Val Pro Pro Phe Asp Pro Phe Asn His Ser Gly Leu Gly
225                               725                               730                               735
227 tgg acg ttc gac cgc gca gag gcg cag aag ctg atc gag gcg ctc ggg      2434
228 Trp Thr Phe Asp Arg Ala Glu Ala Gln Lys Leu Ile Glu Ala Leu Gly
229                               740                               745                               750
231 cac tgc ctc cgc acc tac cgg gac tac aag gag agc tgg agg ggg ctc      2482
232 His Cys Leu Arg Thr Tyr Arg Asp Tyr Lys Glu Ser Trp Arg Gly Leu
233                               755                               760                               765
235 cag gag cgc ggc atg tgc cag gac ttc agc tgg gag cat gcc gcc aag      2530
236 Gln Glu Arg Gly Met Ser Gln Asp Phe Ser Trp Glu His Ala Ala Lys
237 770                               775                               780                               785
239 ctc tac gag gac gtc ctc gtc aag gcc aag tac cag tgg tgaacgctag      2579
240 Leu Tyr Glu Asp Val Leu Val Lys Ala Lys Tyr Gln Trp
241                               790                               795
243 ctgctagccg gtccagcccc gcatgcgtgc atgacaggat ggaattgcgc attgcgcacg 2639
245 caggaagggtg ccatggagcg ccggcatccg cgaagtacag tgacatgagg tgtgtgtggt 2699
247 tgagacgctg attccgatct ggtccgtagc agagtagagc ggaggtaggg aagcgctcct 2759
249 tgttacaggt atatgggaat gttgttaact tggtattgta atttgttatg ttgtgtgcat 2819
251 tattacagag ggcaacgata tgcgcggcg caccggccca actgttgggc cggtcgcaca 2879
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257 <211> LENGTH: 798
258 <212> TYPE: PRT
259 <213> ORGANISM: Triticum aestivum
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263 1 5 10 15
265 Ala Ser Pro Gly Arg Ser Arg Arg Arg Thr Arg Val Ser Ala Ser Pro
266 20 25 30
268 Pro His Thr Gly Ala Gly Arg Leu His Trp Pro Pro Ser Pro Pro Gln
269 35 40 45

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271 Arg Thr Ala Arg Asp Gly Ala Val Ala Ala Arg Ala Ala Gly Lys Lys
272      50                      55                      60
274 Asp Ala Gly Ile Asp Asp Ala Ala Pro Ala Arg Gln Pro Arg Ala Leu
275 65                      70                      75                      80
277 Arg Gly Gly Ala Ala Thr Lys Val Ala Glu Arg Arg Asp Pro Val Lys
278                      85                      90                      95
280 Thr Leu Asp Arg Asp Ala Ala Glu Gly Gly Ala Pro Ser Pro Pro Ala
281                      100                      105                      110
283 Pro Arg Gln Glu Asp Ala Arg Leu Pro Ser Met Asn Gly Met Pro Val
284                      115                      120                      125
286 Asn Gly Glu Asn Lys Ser Thr Gly Gly Gly Gly Ala Thr Lys Asp Ser
287      130                      135                      140
289 Gly Leu Pro Ala Pro Ala Arg Ala Pro Gln Pro Ser Ser Gln Asn Arg
290 145                      150                      155                      160
292 Val Pro Val Asn Gly Glu Asn Lys Ala Asn Val Ala Ser Pro Pro Thr
293                      165                      170                      175
295 Ser Ile Ala Glu Val Ala Ala Pro Asp Pro Ala Ala Thr Ile Ser Ile
296                      180                      185                      190
298 Ser Asp Lys Ala Pro Glu Ser Val Val Pro Ala Glu Lys Ala Pro Pro
299                      195                      200                      205
301 Ser Ser Gly Ser Asn Phe Val Pro Ser Ala Ser Ala Pro Gly Ser Asp
302      210                      215                      220
304 Thr Val Ser Asp Val Glu Leu Glu Leu Lys Lys Gly Ala Val Ile Val
305 225                      230                      235                      240
307 Lys Glu Ala Pro Asn Pro Lys Ala Leu Ser Pro Pro Ala Ala Pro Ala
308                      245                      250                      255
310 Val Gln Gln Asp Leu Trp Asp Phe Lys Lys Tyr Ile Gly Phe Glu Glu
311                      260                      265                      270
313 Pro Val Glu Ala Lys Asp Asp Gly Arg Ala Val Ala Asp Asp Ala Gly
314      275                      280                      285
316 Ser Phe Glu His His Gln Asn His Asp Ser Gly Pro Leu Ala Gly Glu
317      290                      295                      300
319 Asn Val Met Asn Val Val Val Val Ala Ala Glu Cys Ser Pro Trp Cys
320 305                      310                      315                      320
322 Lys Thr Gly Gly Leu Gly Asp Val Ala Gly Ala Leu Pro Lys Ala Leu
323                      325                      330                      335
325 Ala Lys Arg Gly His Arg Val Met Val Val Val Pro Arg Tyr Gly Asp
326      340                      345                      350
328 Tyr Glu Glu Ala Tyr Asp Val Gly Val Arg Lys Tyr Tyr Lys Ala Ala
329      355                      360                      365
331 Gly Gln Asp Met Glu Val Asn Tyr Phe His Ala Tyr Ile Asp Gly Val
332      370                      375                      380
334 Asp Phe Val Phe Ile Asp Ala Pro Leu Phe Arg His Arg Gln Glu Asp
335 385                      390                      395                      400
337 Ile Tyr Gly Gly Ser Arg Gln Glu Ile Met Lys Arg Met Ile Leu Phe
338      405                      410                      415
340 Cys Lys Ala Ala Val Glu Val Pro Trp His Val Pro Cys Gly Gly Val
341      420                      425                      430
343 Pro Tyr Gly Asp Gly Asn Leu Val Phe Ile Ala Asn Asp Trp His Thr

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Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

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L:12 M:270 C: Current Application Number differs, Replaced Current Application Number

L:1910 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9

L:2088 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10

L:3664 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:53

L:3686 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54